

SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.
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 Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose
 Pyrophosphorylase

<130> UF.371XC1

<140> 10/569,000

<141> 2006-10-10

<150> PCT/US2004/026965

<151> 2004-08-18

<150> 60/496,188

<151> 2003-08-18

<160> 44

<170> PatentIn version 3.5

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<212> DNA

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Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
              35              40              45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
              50              55              60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65              70              75              80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
              85              90              95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
              100             105             110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
              115             120             125

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 Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val
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 Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met
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 Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys
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 Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu
 225 230 235 240
 Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile
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 Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe
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 Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser
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 Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr
 325 330 335
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 Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly
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 Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile

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Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile		
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Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile
35        40        45

Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys
50        55        60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp
65        70        75        80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val
85        90        95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala
100       105       110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val
115       120       125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr
130       135       140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val
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Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr
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Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val

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		355					360					365			
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Ile	Glu	Asp	Ser	Leu	Leu	Met	Gly	Ala	Asp	Tyr	Tyr	Glu	Thr	Glu	Ala
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Gly	Asp	Asn	Val	Lys	Ile	Leu	Asn	Ala	Asp	Asn	Val	Gln	Glu	Ala	Ala
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Met	Glu	Thr	Asp	Gly	Tyr	Phe	Ile	Lys	Gly	Gly	Ile	Val	Thr	Val	Ile
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1428

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Asp	Ser	Gln	Thr	Tyr	Leu	Asn	Pro	Gln	Ala	His	Asp	Ser	Val	Leu	Gly	35	40	45	
Ile	Ile	Leu	Gly	Gly	Gly	Ala	Gly	Thr	Arg	Leu	Tyr	Pro	Leu	Thr	Lys	50	55	60	
Lys	Arg	Ala	Lys	Pro	Ala	Val	Pro	Leu	Gly	Ala	Asn	Tyr	Arg	Leu	Ile	65	70	75	80
Asp	Ile	Pro	Val	Ser	Asn	Cys	Leu	Asn	Ser	Asn	Ile	Ser	Lys	Ile	Tyr	85	90	95	
Val	Leu	Thr	Gln	Phe	Asn	Ser	Ala	Ser	Leu	Asn	Arg	His	Leu	Ser	Arg	100	105	110	
Ala	Tyr	Gly	Ser	Asn	Ile	Gly	Gly	Tyr	Lys	Asn	Glu	Gly	Phe	Val	Glu	115	120	125	
Val	Leu	Ala	Ala	Gln	Gln	Ser	Pro	Asp	Asn	Pro	Asn	Trp	Phe	Gln	Gly	130	135	140	
Thr	Ala	Asp	Ala	Val	Arg	Gln	Tyr	Leu	Trp	Leu	Phe	Glu	Glu	His	Asn	145	150	155	160
Val	Met	Glu	Phe	Leu	Ile	Leu	Ala	Gly	Asp	His	Leu	Tyr	Arg	Met	Asp	165	170	175	
Tyr	Glu	Lys	Phe	Ile	Gln	Ala	His	Arg	Glu	Thr	Asn	Ala	Asp	Ile	Thr	180	185	190	
Val	Ala	Ala	Leu	Pro	Met	Asp	Glu	Lys	Arg	Ala	Thr	Ala	Phe	Gly	Leu	195	200	205	
Met	Lys	Ile	Asp	Glu	Glu	Gly	Arg	Ile	Ile	Glu	Phe	Ala	Glu	Lys	Pro	210	215	220	
Lys	Gly	Glu	Gln	Leu	Lys	Ala	Met	Met	Val	Asp	Thr	Thr	Ile	Leu	Gly	225	230	235	240


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Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
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Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
      275                      280                      285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
      290                      295                      300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
      305                      310                      315                      320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
      325                      330                      335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
      340                      345                      350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
      355                      360                      365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
      370                      375                      380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
      385                      390                      395                      400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
      405                      410                      415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
      420                      425                      430

Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala
      435                      440                      445

Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val
      450                      455                      460

Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
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Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala
1           5           10           15

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      20                      25                      30

Asp Ser Gln Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
      35                      40                      45

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
      50                      55                      60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
      65                      70                      75                      80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
      85                      90                      95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
      100                      105                      110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
      115                      120                      125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
      130                      135                      140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
      145                      150                      155                      160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
      165                      170                      175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
      180                      185                      190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
      195                      200                      205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
      210                      215                      220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
      225                      230                      235                      240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
      245                      250                      255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
      260                      265                      270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
      275                      280                      285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
      290                      295                      300

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Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
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Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
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Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
340 345 350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
355 360 365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
370 375 380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
385 390 395 400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
405 410 415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
420 425 430

Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala
435 440 445

Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val
450 455 460

Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
465 470 475

<210> 9

<211> 1428

<212> DNA

<213> zea mays

<400> 9

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caagctcatg atagtgttct tggaatcatt ctgggaggtg gtgctgggac tagattgtac 180

cccttgacaa agaagcgtgc caagcctgca gtgccattgg gtgccaacta tagactgatt 240

gatattcctg tcagcaattg tctcaacagc aacatatcca agatctatgt gctaacgcaa 300

tttaactctg cttccctcaa ccgtcacctc tcaagagcct acgggagcaa cattggaggg 360

tacaagaatg aagggtttgt tgaagtctta gctgcacagc agagcccaga taatccaaac 420

tggtttcagg gtactgcaga tgctgtaagg cagtacttgt gggtgtttga ggagcataat 480

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gtgatggaat ttctaattct tgctggcgat cacctgtacc ggatggacta tgaaaagttc 540
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aaacgtgcaa ctgcatttgg cctcatgaaa attgatgaag aaggaggat cattgagttt 660
gctgagaaac cgaaaggaga gcagttgaaa gcaatgatgg ttgacaccac catacttggc 720
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agcaaagatg taatgcttca gctcctccgt gaacaatttc ctgaagccaa tgactttgga 840
agtgagggtta ttccagggtgc aaccagcatt ggaaagaggg ttcagggtta tctgtatgat 900
ggttactggg aagatatcgg taccattgcg gcattttata atgcaaactt gggaataacc 960
aagaagccaa taccagattt cagcttctat gaccgttttg ctccaattta tacacaacct 1020
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gctgataaaa aactccttgc cgaaaaaggt ggcattccta ttggtattgg gaaaaattca 1260
tgcatcagga gagcaatcat tgacaagaat gctcgaattg gagacaatgt taagatactc 1320
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<210> 10
<211> 476
<212> PRT
<213> zea mays

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<400> 10
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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn
20           25           30

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Asp Ser Glu Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly
35           40           45

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```

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
50           55           60

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Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
65           70           75           80

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Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
      85                      90                      95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
      100                    105                    110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
      115                    120                    125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
      130                    135                    140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
      145                    150                    155                    160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
      165                    170                    175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr
      180                    185                    190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu
      195                    200                    205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro
      210                    215                    220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
      225                    230                    235                    240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
      245                    250                    255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln
      260                    265                    270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
      275                    280                    285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
      290                    295                    300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
      305                    310                    315                    320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile
      325                    330                    335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
      340                    345                    350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
      355                    360                    365

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Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
 370 375 380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
 385 390 395 400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile
 405 410 415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
 420 425 430

Ile Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala
 435 440 445

Ala Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val
 450 455 460

Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
 465 470 475

<210> 11

<211> 1582

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

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 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt	147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe	
35 40 45	
ggg ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct	195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala	
50 55 60	
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat	243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr	
65 70 75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga	291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly	
80 85 90	
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct	339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	
95 100 105 110	
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115 120 125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	

240	245	250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat			819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
255	260	265	270
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat			867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
	275	280	285
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc			915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe			
	290	295	300
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta			963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu			
	305	310	315
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cat agt			1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser			
	320	325	330
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc			1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile			
	335	340	345
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag			1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys			
	355	360	365
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc			1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys			
	370	375	380
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc			1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile			
	385	390	395
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att			1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile			
	400	405	410
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg			1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val			
	415	420	425
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta			1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu			
	435	440	445
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata			1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile			
	450	455	460
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg			1443

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Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
    465                      470                      475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg    1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                      485                      490

tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca    1539
Tyr Ser Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala
    495                      500                      505                      510

acc atc aac gat ggg tct gtc ata tagatcggct gcgtktgcg    1582
Thr Ile Asn Asp Gly Ser Val Ile
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<210> 12
 <211> 518
 <212> PRT
 <213> Zea mays

<400> 12

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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    20                      25                      30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
    35                      40                      45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                      55                      60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
    65                      70                      75                      80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
    85                      90                      95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
    100                     105                     110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
    115                     120                     125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130                     135                     140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
    145                     150                     155                     160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
    165                     170                     175

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Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser
 485 490 495

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 500 505 510

Asn Asp Gly Ser Val Ile
 515

<210> 13

<211> 1582

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1578)

<223> k = g or t.

<400> 13

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 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

										35											40											45												
ggt	ggt	aga	ggt	gct	gca	act	aca	caa	tgt	att	ctt	acc	tca	gat	gct	195																												
Gly	Gly	Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala																													
										50											55											60												
tgt	cct	gaa	act	ctt	cat	tct	caa	aca	cag	tcc	tct	agg	aaa	aat	tat	243																												
Cys	Pro	Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr																													
										65											70											75												
gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291																												
Ala	Asp	Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly																													
										80											85											90												
tct	cag	ctc	ttt	cct	ctg	aca	agc	aca	aga	gct	acg	cct	gct	gta	cct	339																												
Ser	Gln	Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro																													
										95											100											105											110	
ggt	gga	gga	tgt	tac	agg	ctt	att	gat	atc	cct	atg	agt	aac	tgc	ttc	387																												
Val	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe																													
										115											120											125												
aac	agt	ggt	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act	435																												
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr																													
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tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483																												
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn																													
										145											150											155												
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531																												
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu																													
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gag	cca	gct	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579																												
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe																													
										175											180											185											190	
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627																												
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile																													
										195											200											205												
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675																												
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu																													
										210											215											220												
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723																												
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala																													
										225											230											235												
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771																												
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp																													
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His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	
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Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	
				275					280					285		
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	
			290					295					300			
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	
		305					310					315				
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	tay	agt	1011
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser	
	320					325				330						
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	
335					340					345					350	
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag	1107
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	
				355					360					365		
ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc	1155
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	
			370					375					380			
ttg	cct	ccg	acg	caa	ttg	gac	aag	tgc	aag	atg	aaa	tat	gca	ttt	atc	1203
Leu	Pro	Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile	
		385					390					395				
tca	gat	ggt	tgc	tta	ctg	aga	gaa	tgc	aac	atc	gag	cat	tct	gtg	att	1251
Ser	Asp	Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile	
	400					405					410					
gga	gtc	tgc	tca	cgt	gtc	agc	tct	gga	tgt	gaa	ctc	aag	gac	tcc	gtg	1299
Gly	Val	Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val	
415					420					425					430	
atg	atg	gga	gcg	gac	atc	tat	gaa	act	gaa	gaa	gaa	gct	tca	aag	cta	1347
Met	Met	Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu	
				435					440					445		
ctg	tta	gct	ggg	aag	gtc	ccr	gtt	gga	ata	gga	agg	aac	aca	aag	ata	1395
Leu	Leu	Ala	Gly	Lys	Val	Pro	Val	Gly	Ile	Gly	Arg	Asn	Thr	Lys	Ile	
			450					455					460			
agg	aac	tgt	atc	att	gac	atg	aat	gct	agg	att	ggg	aag	aac	gtg	gtg	1443
Arg	Asn	Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	Lys	Asn	Val	Val	
		465					470					475				

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 ile thr asn ser lys gly ile gln glu ala asp his pro glu glu gly
 480 485 490

tac tcg tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca 1539
 tyr ser tyr tyr ile arg ser gly ile val val ile leu lys asn ala
 495 500 505 510

acc atc aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1582
 thr ile asn asp gly ser val ile
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<211> 518

<212> PRT

<213> Zea mays

<400> 14

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190

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Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
    195                      200                      205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
    210                      215                      220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
    225                      230                      235                      240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
    245                      250                      255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
    260                      265                      270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
    275                      280                      285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
    290                      295                      300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
    305                      310                      315                      320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
    325                      330                      335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
    340                      345                      350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
    355                      360                      365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
    370                      375                      380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
    385                      390                      395                      400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
    405                      410                      415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
    420                      425                      430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
    435                      440                      445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
    450                      455                      460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
    465                      470                      475                      480

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Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Ser
 485 490 495

Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 500 505 510

Asn Asp Gly Ser Val Ile
 515

<210> 15

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1572)

<223> k = g or t.

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 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

Gly	Gly	Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala		
			50					55					60				
tgt	cct	gaa	act	ctt	cat	tct	caa	aca	cag	tcc	tct	agg	aaa	aat	tat	243	
Cys	Pro	Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr		
		65					70					75					
gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291	
Ala	Asp	Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly		
	80					85					90						
tct	cag	ctc	ttt	cct	ctg	aca	agc	aca	aga	gct	acg	cct	gct	gta	cct	339	
Ser	Gln	Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro		
	95				100				105						110		
gtt	gga	gga	tgt	tac	agg	ctt	att	gat	atc	cct	atg	agt	aac	tgc	ttc	387	
Val	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe		
			115					120					125				
aac	agt	ggt	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act	435	
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr		
		130						135					140				
tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483	
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn		
		145					150					155					
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531	
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu		
	160					165					170						
gag	cca	gct	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579	
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe		
	175				180				185						190		
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627	
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile		
			195					200					205				
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675	
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu		
			210					215					220				
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723	
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala		
		225					230					235					
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771	
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp		
		240				245					250						
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819	
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp		
				255		260				265					270		

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Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser	
320 325 330	
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Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	
435 440 445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata	1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile	
450 455 460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg	1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val	
465 470 475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg	1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly	
480 485 490	

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
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aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576
 Asn Asp Gly Ser Val Ile
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<210> 16

<211> 516

<212> PRT

<213> Zea mays

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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205

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Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210                215                220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                230                235                240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245                250                255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
                260                265                270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
                275                280                285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
290                295                300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                310                315                320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
                325                330                335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
                340                345                350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
355                360                365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
370                375                380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                390                395                400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                405                410                415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
                420                425                430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
435                440                445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
450                455                460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                470                475                480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                485                490                495

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Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510

Gly Ser Val Ile
 515

<210> 17

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (540)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1572)

<223> k = g or t.

<400> 17

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 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct	195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala	
50 55 60	
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat	243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr	
65 70 75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga	291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly	
80 85 90	
tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct	339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro	
95 100 105 110	
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115 120 125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca ccn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	

255	260	265	270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867			
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp				
275 280 285				
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915			
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe				
290 295 300				
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963			
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu				
305 310 315				
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt	1011			
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser				
320 325 330				
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059			
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile				
335 340 345 350				
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107			
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys				
355 360 365				
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155			
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys				
370 375 380				
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Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile				
385 390 395				
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251			
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile				
400 405 410				
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299			
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val				
415 420 425 430				
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347			
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu				
435 440 445				
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata	1395			
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile				
450 455 460				
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg	1443			
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val				
465 470 475				
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg	1491			


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Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480                               485                               490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                               500                               505                               510

aac gat ggg tct gtc ata tagatcggct gcgktgtcg 1576
Asn Asp Gly Ser Val Ile
                               515

<210> 18
<211> 516
<212> PRT
<213> Zea mays

<400> 18

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
 1                               5                               10                               15

Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
                20                               25                               30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
    35                               40                               45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                               55                               60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
    65                               70                               75                               80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
                85                               90                               95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
    100                               105                               110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
    115                               120                               125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
    130                               135                               140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
    145                               150                               155                               160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                               170                               175

Pro Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
    180                               185                               190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile

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195					200					205					
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
210					215					220					
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
225					230					235					240
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
				245					250					255	
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn
			260					265					270		
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala
		275					280					285			
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys
	290					295				300					
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp
305					310					315					320
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser	Val	Gln
				325					330					335	
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser
			340					345					350		
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp
		355					360					365			
Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	Leu	Pro
	370					375					380				
Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile	Ser	Asp
385					390					395					400
Gly	Cys	Leu	Leu	Arg	Glu	Cys	Asn	Ile	Glu	His	Ser	Val	Ile	Gly	Val
				405					410					415	
Cys	Ser	Arg	Val	Ser	Ser	Gly	Cys	Glu	Leu	Lys	Asp	Ser	Val	Met	Met
			420					425					430		
Gly	Ala	Asp	Ile	Tyr	Glu	Thr	Glu	Glu	Glu	Ala	Ser	Lys	Leu	Leu	Leu
	435						440					445			
Ala	Gly	Lys	Val	Pro	Val	Gly	Ile	Gly	Arg	Asn	Thr	Lys	Ile	Arg	Asn
	450					455					460				
Cys	Ile	Ile	Asp	Met	Asn	Ala	Arg	Ile	Gly	Lys	Asn	Val	Val	Ile	Thr
465					470					475					480
Asn	Ser	Lys	Gly	Ile	Gln	Glu	Ala	Asp	His	Pro	Glu	Glu	Gly	Tyr	Tyr
				485					490					495	

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510

Gly Ser Val Ile
 515

<210> 19
 <211> 1576
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (10)..(1563)
 <223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>
 <221> variation
 <222> (267)
 <223> k = g or t; amino acid 86 = Ala.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1209)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
 <221> variation
 <222> (1371)
 <223> h = a or c or t/u.

<220>
 <221> variation
 <222> (1572)
 <223> k = g or t.

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 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
 1 5 10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln	Ile	Arg	Ser	Cys	Glu	Gly	Asp	Gly	Ile	Asp	Arg	Leu	Glu	Lys	Leu	
15					20				25						30	
agt	att	ggg	ggc	aga	aag	cag	gag	aaa	gct	ttg	aga	aat	agg	tgc	ttt	147
Ser	Ile	Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	
				35				40						45		
ggt	ggt	aga	gtt	gct	gca	act	aca	caa	tgt	att	ctt	acc	tca	gat	gct	195
Gly	Gly	Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	
			50					55					60			
tgt	cct	gaa	act	ctt	cat	tct	caa	aca	cag	tcc	tct	agg	aaa	aat	tat	243
Cys	Pro	Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	
		65					70					75				
gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291
Ala	Asp	Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	
	80					85				90						
tct	cag	ctc	ttt	cct	ctg	aca	agc	aca	aga	gct	acg	cct	gct	gta	cct	339
Ser	Gln	Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	
	95				100					105					110	
gtt	gga	gga	tgt	tac	agg	ctt	att	gat	atc	cct	atg	agt	aac	tgc	ttc	387
Val	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	
			115					120						125		
aac	agt	ggt	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act	435
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	
		130					135						140			
tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	
		145					150						155			
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	
	160					165				170						
gag	cca	gct	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	
	175				180					185					190	
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	
			195					200						205		
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	
		210						215					220			
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	
		225				230						235				

cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca cay ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251
Ser His Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	
435 440 445	
ctg tta gct ggg aag gtc ccr ath gga ata gga agg aac aca aag ata	1395
Leu Leu Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile	
450 455 460	

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 20

<211> 516

<212> PRT

<213> Zea mays

<400> 20

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160

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Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
      165                      170                      175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
      180                      185                      190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
      195                      200                      205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
      210                      215                      220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
      225                      230                      235                      240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
      245                      250                      255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
      260                      265                      270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
      275                      280                      285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
      290                      295                      300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
      305                      310                      315                      320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
      325                      330                      335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
      340                      345                      350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
      355                      360                      365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
      370                      375                      380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser His
      385                      390                      395                      400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
      405                      410                      415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
      420                      425                      430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
      435                      440                      445

Ala Gly Lys Val Pro Ile Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn

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      450              455              460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465              470              475              480
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
      485              490              495
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
      500              505              510
Gly Ser Val Ile
      515

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<210> 21
<211> 1576
<212> DNA
<213> Zea mays

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<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
      heat stable

```

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<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

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```

<220>
<221> variation
<222> (321)
<223> n = a or g or c or t/u, unknown, or other.

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<220>
<221> variation
<222> (1008)
<223> y = c or t.

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<220>
<221> variation
<222> (1368)
<223> r = a or g; amino acid 453 = Pro.

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```

<220>
<221> variation
<222> (1572)
<223> k = g or t.

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<400> 21
ggaggagat atg cag ttt gca ctt gca ttg gac acg aac tca ggt cct cac 51
      Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His
      1              5              10

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta	99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu	
15 20 25 30	
agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt	147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe	
35 40 45	
ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct	195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala	
50 55 60	
tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat	243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr	
65 70 75	
gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga	291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly	
80 85 90	
tct cag ctc ttt cct ctg aca agc aca acn gct acg cct gct gta cct	339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro	
95 100 105 110	
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115 120 125	
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act	435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa	531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
160 165 170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	

225	230	235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp 240 245 250			771
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp 255 260 265 270			819
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp 275 280 285			867
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe 290 295 300			915
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu 305 310 315			963
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser 320 325 330			1011
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile 335 340 345 350			1059
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys 355 360 365			1107
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys 370 375 380			1155
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile 385 390 395			1203
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile 400 405 410			1251
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val 415 420 425 430			1299
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu 435 440 445			1347
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata			1395

Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
 450 455 460

 agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475

 atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

 tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510

 aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 22

<211> 516

<212> PRT

<213> Zea mays

<400> 22

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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 Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30

 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

 Leu Phe Pro Leu Thr Ser Thr Thr Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140

 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala

145		150		155		160
Asp Gly Ser Val	Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro					
	165			170		175
Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp						
	180			185		190
Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile						
	195			200		205
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln						
	210			215		220
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val						
	225			230		240
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr						
	245			250		255
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn						
	260			265		270
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala						
	275			280		285
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys						
	290			295		300
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp						
	305			310		320
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln						
	325			330		335
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser						
	340			345		350
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp						
	355			360		365
Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro						
	370			375		380
Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp						
	385			390		400
Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val						
	405			410		415
Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met						
	420			425		430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu						
	435			440		445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
 485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510

Gly Ser Val Ile
 515

<210> 23

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1389)

<223> h = a or c or t/u.

<220>

<221> variation

<222> (1572)

<223> k = g or t.

<400> 23

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Met	Gln	Phe	Ala	Leu	Ala	Leu	Asp	Thr	Asn	Ser	Gly	Pro	His			
1					5				10							
cag	ata	aga	tct	tgt	gag	ggg	gat	ggg	att	gac	agg	ttg	gaa	aaa	tta	99
Gln	Ile	Arg	Ser	Cys	Glu	Gly	Asp	Gly	Ile	Asp	Arg	Leu	Glu	Lys	Leu	
15					20				25						30	
agt	att	ggg	ggc	aga	aag	cag	gag	aaa	gct	ttg	aga	aat	agg	tgc	ttt	147
Ser	Ile	Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	
				35					40					45		
ggg	ggg	aga	gtt	gct	gca	act	aca	caa	tgt	att	ctt	acc	tca	gat	gct	195
Gly	Gly	Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	
			50					55					60			
tgt	cct	gaa	act	ctt	cat	tct	caa	aca	cag	tcc	tct	agg	aaa	aat	tat	243
Cys	Pro	Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	
		65					70					75				
gct	gat	gca	aac	cgt	gta	tct	gck	atc	att	ttg	ggc	gga	ggc	act	gga	291
Ala	Asp	Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	
	80					85					90					
tct	cag	ctc	ttt	cct	ctg	aca	agc	aca	aga	gct	acg	cct	gct	gta	cct	339
Ser	Gln	Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	
	95				100					105					110	
gtt	gga	gga	tgt	tac	agg	ctt	att	gat	atc	cct	atg	agt	aac	tgc	ttc	387
Val	Gly	Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	
			115					120						125		
aac	agt	ggg	ata	aat	aag	ata	ttt	gtg	atg	agt	cag	ttc	aat	tct	act	435
Asn	Ser	Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	
			130				135						140			
tgc	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	
		145					150					155				
ttt	gct	gat	gga	tct	gta	cag	gtat	tta	gcg	gct	aca	caa	atg	cct	gaa	531
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	
	160					165					170					
gag	cca	gct	gga	tgg	ttc	cag	ggg	aca	gca	gac	tct	atc	aga	aaa	ttt	579
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	
	175				180					185					190	
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	
			195					200						205		
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	
			210				215						220			

gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	
385 390 395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att	1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile	
400 405 410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg	1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val	
415 420 425 430	
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta	1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu	
435 440 445	

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac ath aag ata 1395
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile
 450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 24

<211> 516

<212> PRT

<213> Zea mays

<400> 24

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 20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125

Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140


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Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
145                150                155                160

Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
                165                170                175

Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
                180                185                190

Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
                195                200                205

Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
                210                215                220

Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
225                230                235                240

Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
                245                250                255

Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
                260                265                270

Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
                275                280                285

Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
                290                295                300

Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
305                310                315                320

Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
                325                330                335

Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
                340                345                350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
                355                360                365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
                370                375                380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                390                395                400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                405                410                415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
                420                425                430

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Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Ile Lys Ile Arg Asn
 450 455 460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
 485 490 495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510

Gly Ser Val Ile
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<210> 25

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
 heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (657)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1572)

<223> k = g or t.

<400> 25

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        1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
        35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
        50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
      80             85             90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
      95             100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
        115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
        130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145             150             155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160             165             170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe
        175             180             185             190

atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att 627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile
        195             200             205

gta atc ttg agt ggc gat cag ctt tat ccn atg aat tac atg gaa ctt 675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu

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210	215	220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct			723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala			
225	230	235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat			771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp			
240	245	250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat			819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
255	260	265	270
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat			867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
275	280	285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc			915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe			
290	295	300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta			963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu			
305	310	315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt			1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser			
320	325	330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc			1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile			
335	340	345	350
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag			1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys			
355	360	365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc			1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys			
370	375	380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc			1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile			
385	390	395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att			1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile			
400	405	410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg			1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val			
415	420	425	430
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta			1347

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Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
      435                      440                      445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
      450                      455                      460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
      465                      470                      475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
      480                      485                      490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
      495                      500                      505                      510

aac gat ggg tct gtc ata tagatcggct gcgktgtcg 1576
Asn Asp Gly Ser Val Ile
      515

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<210> 26
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 <213> Zea mays

<400> 26

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      20                      25                      30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
      35                      40                      45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
      50                      55                      60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
      65                      70                      75                      80

Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
      85                      90                      95

Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
      100                     105                     110

Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
      115                     120                     125

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Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175
 Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205
 Leu Ser Gly Asp Gln Leu Tyr Pro Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
 290 295 300
 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met

420	425	430
Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu		
435	440	445
Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn		
450	455	460
Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr		
465	470	475
Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr		
485	490	495
Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp		
500	505	510
Gly Ser Val Ile		
515		

<210> 27

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (540)

<223> n = a or g or c or t/u, unknown, or other.

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<222> (1008)

<223> y = c or t.

<220>

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<222> (1287)

<223> y = c or t.

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<221> variation

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<223> r = a or g; amino acid 453 = Pro.

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<221> variation

<222> (1572)

<223> k = g or t.

<400> 27

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          1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
          35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
          50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
          65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
          80             85             90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
          95             100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
          115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
          130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
          145             150             155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
          160             165             170

gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe

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175	180	185	190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att				627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	195	200	205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt				675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	210	215	220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct				723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	225	230	235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat				771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	240	245	250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat				819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	255	260	265	270
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat				867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	275	280	285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc				915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	290	295	300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta				963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	305	310	315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat cay agt				1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser	320	325	330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc				1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	335	340	345	350
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag				1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	355	360	365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc				1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	370	375	380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc				1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	385	390	395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att				1251

Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
 400 405 410
 gga gtc tgc tca cgt gtc agc tct gga tgt gaa tty aag gac tcc gtg 1299
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val
 415 420 425 430
 atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
 435 440 445
 ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
 450 455 460
 agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475
 atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490
 tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
 495 500 505 510
 aac gat ggg tct gtc ata tagatcggct gcgktgctg 1576
 Asn Asp Gly Ser Val Ile
 515

<210> 28
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 <212> PRT
 <213> Zea mays

<400> 28

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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 Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
 20 25 30
 Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
 35 40 45
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
 50 55 60
 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln

85					90					95					
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
			100					105					110		
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
			115				120					125			
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
			130				135					140			
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala
					150					155					160
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro
				165					170					175	
Val	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
			180					185					190		
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
			195				200					205			
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
			210				215					220			
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
					230					235					240
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
				245					250					255	
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn
			260					265					270		
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala
			275				280					285			
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys
			290				295				300				
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp
					310					315					320
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser	Val	Gln
				325					330					335	
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser
				340				345					350		
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp
			355				360					365			
Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	Leu	Pro
					375						380				

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Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                390                395                400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                405                410                415

Cys Ser Arg Val Ser Ser Gly Cys Glu Phe Lys Asp Ser Val Met Met
                420                425                430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
                435                440                445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
                450                455                460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                470                475                480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
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Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
                500                505                510

Gly Ser Val Ile
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<210> 29
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunk-2 gene revertant form, modified to be
        heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (981)
<223> r = g or a.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

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<220>
 <221> variation
 <222> (1086)
 <223> n = a or g or c or t/u, unknown, or other.

<220>
 <221> variation
 <222> (1197)
 <223> n = a or g or c or t/u, unknown, or other.

<220>
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 <223> r = a or g; amino acid 453 = Pro.

<220>
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 <223> k = g or t.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
 115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

130	135	140	
tct ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac			483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn			
145	150	155	
ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa			531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu			
160	165	170	
gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt			579
Glu Pro Ala Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe			
175	180	185	190
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att			627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile			
195	200	205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt			675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu			
210	215	220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct			723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala			
225	230	235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat			771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp			
240	245	250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat			819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp			
255	260	265	270
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat			867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp			
275	280	285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc			915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe			
290	295	300	
aag aaa gat gca ctt tta gac ctt ctg aag tca aaa tat act caa tta			963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu			
305	310	315	
cat gac ttt gga tct aar atc ctg cca aga gct gta cta gat cay agt			1011
His Asp Phe Gly Ser Lys Ile Leu Pro Arg Ala Val Leu Asp His Ser			
320	325	330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc			1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile			
335	340	345	350
aaa tca ttc ttt gat gca aac ttg gtn ctg act gag cag cct tcc aag			1107

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Lys Ser Phe Phe Asp Ala Asn Leu Val Leu Thr Glu Gln Pro Ser Lys
      355                      360                      365

ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
      370                      375                      380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
      385                      390                      395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
      400                      405                      410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
      415                      420                      425                      430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
      435                      440                      445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
      450                      455                      460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
      465                      470                      475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
      480                      485                      490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
      495                      500                      505                      510

aac gat ggg tct gtc ata tagatcggct gcgktgcg 1576
Asn Asp Gly Ser Val Ile
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<210> 30

<211> 516

<212> PRT

<213> Zea mays

<400> 30

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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile

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20					25					30					
Gly	Gly	Arg	Lys	Gln	Glu	Lys	Ala	Leu	Arg	Asn	Arg	Cys	Phe	Gly	Gly
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Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro
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Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp
		65					70					75			
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln
				85					90					95	
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly
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Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser
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Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu
		130					135					140			
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala
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Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro
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Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp
			180					185					190		
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile
		195					200					205			
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln
		210					215					220			
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val
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Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr
				245					250					255	
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn
			260					265					270		
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala
		275					280					285			
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys
		290					295					300			
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp
		305					310					315			320

Phe Gly Ser Lys Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
 Phe Phe Asp Ala Asn Leu Val Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
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<210> 31

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<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

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<222> (1572)

<223> k = g or t.

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

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10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99

Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu

15

20

25

30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147

Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe

35

40

45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195

Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala

50

55

60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243

Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr

65

70

75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291

Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly

80

85

90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339

Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro

95

100

105

110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387

Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe

115

120

125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435

Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

130

135

140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483

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Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu		
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Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe		
	175				180				185						190		
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Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile		
				195					200					205			
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675	
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu		
			210					215					220				
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723	
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala		
		225					230					235					
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771	
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp		
	240					245					250						
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggc	gct	gat	819	
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp		
	255				260				265						270		
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867	
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp		
				275				280						285			
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915	
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe		
			290					295					300				
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963	
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu		
		305					310					315					
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	tty	agt	1011	
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Phe	Ser		
	320					325					330						
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059	
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile		
	335				340				345						350		
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag	1107	
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys		
				355				360						365			

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ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc 1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
370 375 380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc 1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile
385 390 395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400 405 410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415 420 425 430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
435 440 445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
450 455 460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
465 470 475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
480 485 490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495 500 505 510

aac gat ggg tct gtc ata tagatcggct gcgtktgcg 1576
Asn Asp Gly Ser Val Ile
515

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<210> 32

<211> 516

<212> PRT

<213> Zea mays

<400> 32

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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
20 25 30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly

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35	40	45																	
Arg	Val	Ala	Ala	Thr	Thr	Gln	Cys	Ile	Leu	Thr	Ser	Asp	Ala	Cys	Pro				
50						55					60								
Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp				
65					70					75					80				
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln				
				85					90					95					
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly				
			100					105					110						
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser				
		115					120					125							
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu				
	130					135					140								
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala				
145					150					155					160				
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro				
				165					170					175					
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp				
			180					185					190						
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile				
		195					200					205							
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln				
	210					215					220								
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val				
225					230					235				240					
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr				
				245					250					255					
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn				
			260					265					270						
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala				
		275					280						285						
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys				
	290					295					300								
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp				
305					310					315				320					
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Phe	Ser	Val	Gln				
				325					330					335					

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Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
      340              345              350

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
      355              360              365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
      370              375              380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385              390              395              400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
      405              410              415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
      420              425              430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
      435              440              445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
      450              455              460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465              470              475              480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
      485              490              495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
      500              505              510

Gly Ser Val Ile
      515

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<210> 33

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1572)

<223> k = g or t.

<400> 33

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        1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
        35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
        50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
        65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
        80             85             90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
        95             100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
        115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
        130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
        145             150             155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
        160             165             170

gag cca gct gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt 579

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Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	
175					180					185					190	
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	
				195					200					205		
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	
			210					215					220			
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	
		225					230					235				
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	
	240					245				250						
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggg	gct	gat	819
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	
255				260					265						270	
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	
				275				280						285		
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	
			290				295						300			
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	
		305				310						315				
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	atg	agt	1011
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Met	Ser	
	320				325					330						
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	
335				340				345						350		
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag	1107
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	
			355				360						365			
ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc	1155
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	
			370				375					380				
ttg	cct	ccg	acg	caa	ttg	gac	aag	tgc	aag	atg	aaa	tat	gca	ttt	atc	1203
Leu	Pro	Pro	Thr	Gln	Leu	Asp	Lys	Cys	Lys	Met	Lys	Tyr	Ala	Phe	Ile	
		385				390					395					


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tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
    400                      405                      410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
    415                      420                      425                      430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
                435                      440                      445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
                450                      455                      460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
                465                      470                      475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
    480                      485                      490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
    495                      500                      505                      510

aac gat ggg tct gtc ata tagatcggct gcgktgctg 1576
Asn Asp Gly Ser Val Ile
                515

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<210> 34

<211> 516

<212> PRT

<213> Zea mays

<400> 34

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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                20                      25                      30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
    35                      40                      45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
    50                      55                      60

Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
    65                      70                      75                      80

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Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln	85	90	95
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly	100	105	110
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser	115	120	125
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu	130	135	140
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala	145	150	155
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro	165	170	175
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp	180	185	190
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile	195	200	205
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln	210	215	220
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val	225	230	235
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr	245	250	255
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn	260	265	270
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala	275	280	285
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys	290	295	300
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp	305	310	315
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Met	Ser	Val	Gln	325	330	335
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser	340	345	350
Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys	Phe	Asp	355	360	365
Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys	Leu	Pro			

370

375

380

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Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                390                395                400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                405                410                415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
                420                425                430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
                435                440                445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
                450                455                460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                470                475                480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                485                490                495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
                500                505                510

Gly Ser Val Ile
                515

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<210> 35

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (540)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1008)

<223> y = c or t.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
 <221> variation
 <222> (1572)
 <223> k = g or t.

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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
 115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
 130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
 Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
 145 150 155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531
 Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu
 160 165 170

gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
175 180 185 190	
atc tgg gta ctc gag gat tat tac agt cac aaa tcc att gac aac att	627
Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
gtg cag aaa cat gtc gag gac gat gct gat atc act ata tca tgt gct	723
Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
cct gtt gat gag agc cga gct tct aaa aat ggg cta gtg aag att gat	771
Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
240 245 250	
cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
255 260 265 270	
ttg aat tct atg aga gtt gag acc aac ttc ctg agc tat gct ata gat	867
Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
gat gca cag aaa tat cca tac ctt gca tca atg ggc att tat gtc ttc	915
Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
cat gac ttt gga tct gaa atc ctc cca aga gct gta cta gat tay agt	1011
His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser	
320 325 330	
gtg cag gca tgc att ttt acg ggc tat tgg gag gat gtt gga aca atc	1059
Val Gln Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile	
335 340 345 350	
aaa tca ttc ttt gat gca aac ttg gcc ctc act gag cag cct tcc aag	1107
Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys	
355 360 365	
ttt gat ttt tac gat cca aaa aca cct ttc ttc act gca ccc cga tgc	1155
Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys	
370 375 380	
ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gca ttt atc	1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile	

385	390	395	
tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att			1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile			
400	405	410	
gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg			1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val			
415	420	425	430
atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta			1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu			
435	440	445	
ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata			1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile			
450	455	460	
agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg			1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val			
465	470	475	
atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg			1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly			
480	485	490	
tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc			1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile			
495	500	505	510
aac gat ggg tct gtc ata tagatcggct gcgktg			1576
Asn Asp Gly Ser Val Ile			
515			

<210> 36

<211> 516

<212> PRT

<213> Zea mays

<400> 36

Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile			
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile			
20	25	30	
Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly			
35	40	45	
Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro			
50	55	60	
Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp			

65	70	75	80
Ala Asn Arg Val Ser	Ala Ile Ile Leu	Gly Gly Gly Thr Gly	Ser Gln
85	90	95	
Leu Phe Pro Leu Thr Ser Thr Arg	Ala Thr Pro Ala Val	Pro Val Gly	
100	105	110	
Gly Cys Tyr Arg Leu Ile Asp Ile	Pro Met Ser Asn Cys Phe Asn Ser		
115	120	125	
Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu			
130	135	140	
Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala			
145	150	155	160
Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro			
165	170	175	
Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp			
180	185	190	
Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile			
195	200	205	
Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln			
210	215	220	
Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val			
225	230	235	240
Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr			
245	250	255	
Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn			
260	265	270	
Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala			
275	280	285	
Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys			
290	295	300	
Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp			
305	310	315	320
Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln			
325	330	335	
Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser			
340	345	350	
Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp			
355	360	365	

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Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370                      375                      380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Ala Phe Ile Ser Asp
385                      390                      395                      400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
                      405                      410                      415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
                      420                      425                      430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
                      435                      440                      445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
                      450                      455                      460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                      470                      475                      480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
                      485                      490                      495

Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
                      500                      505                      510

Gly Ser Val Ile
                      515

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<210> 37
<211> 1576
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form, modified to be
      heat stable

<220>
<221> variation
<222> (267)
<223> k = g or t; amino acid 86 = Ala.

<220>
<221> variation
<222> (1008)
<223> y = c or t.

<220>
<221> variation

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<222> (1197)

<223> n = a or g or c or t/u, unknown, or other.

<220>

<221> variation

<222> (1368)

<223> r = a or g; amino acid 453 = Pro.

<220>

<221> variation

<222> (1572)

<223> k = g or t.

<400> 37

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        1             5             10

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
  15             20             25             30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
          35             40             45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
          50             55             60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
          65             70             75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
          80             85             90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
          95             100             105             110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
          115             120             125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
          130             135             140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
          145             150             155

ttt gct gat gga tct gta cag gta tta gcg gct aca caa atg cct gaa 531

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Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu		
	160					165					170						
gag	cca	gct	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579	
Glu	Pro	Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe		
	175				180					185					190		
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627	
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile		
				195					200					205			
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675	
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu		
			210					215					220				
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723	
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala		
		225					230					235					
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771	
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp		
	240					245					250						
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggg	gct	gat	819	
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp		
	255				260					265					270		
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867	
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp		
				275					280					285			
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915	
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe		
			290					295					300				
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963	
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu		
		305				310						315					
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	tay	agt	1011	
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser		
	320					325					330						
gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059	
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile		
	335				340					345					350		
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag	1107	
Lys	Ser	Phe	Phe	Asp	Ala	Asn	Leu	Ala	Leu	Thr	Glu	Gln	Pro	Ser	Lys		
				355				360						365			
ttt	gat	ttt	tac	gat	cca	aaa	aca	cct	ttc	ttc	act	gca	ccc	cga	tgc	1155	
Phe	Asp	Phe	Tyr	Asp	Pro	Lys	Thr	Pro	Phe	Phe	Thr	Ala	Pro	Arg	Cys		
			370					375					380				

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ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
      385                      390                      395

tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
      400                      405                      410

gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
415                      420                      425                      430

atg atg gga gcg gac atc tat gaa act gaa gaa gaa gct tca aag cta 1347
Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
      435                      440                      445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
      450                      455                      460

agg aac tgt atc att gac atg aat gct agg att ggg aag aac gtg gtg 1443
Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
      465                      470                      475

atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
      480                      485                      490

tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
495                      500                      505                      510

aac gat ggg tct gtc ata tagatcggct gcgktgctg 1576
Asn Asp Gly Ser Val Ile
      515

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<210> 38

<211> 516

<212> PRT

<213> Zea mays

<400> 38

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Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His Gln Ile
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Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu Ser Ile
      20                      25                      30

Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe Gly Gly
      35                      40                      45

Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
  50                      55                      60

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Glu	Thr	Leu	His	Ser	Gln	Thr	Gln	Ser	Ser	Arg	Lys	Asn	Tyr	Ala	Asp	65	70	75	80
Ala	Asn	Arg	Val	Ser	Ala	Ile	Ile	Leu	Gly	Gly	Gly	Thr	Gly	Ser	Gln	85	90	95	
Leu	Phe	Pro	Leu	Thr	Ser	Thr	Arg	Ala	Thr	Pro	Ala	Val	Pro	Val	Gly	100	105	110	
Gly	Cys	Tyr	Arg	Leu	Ile	Asp	Ile	Pro	Met	Ser	Asn	Cys	Phe	Asn	Ser	115	120	125	
Gly	Ile	Asn	Lys	Ile	Phe	Val	Met	Ser	Gln	Phe	Asn	Ser	Thr	Ser	Leu	130	135	140	
Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	Phe	Ala	145	150	155	160
Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	Glu	Pro	165	170	175	
Ala	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	Ile	Trp	180	185	190	
Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	Val	Ile	195	200	205	
Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	Val	Gln	210	215	220	
Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	Pro	Val	225	230	235	240
Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	His	Thr	245	250	255	
Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	Leu	Asn	260	265	270	
Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	Asp	Ala	275	280	285	
Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	Lys	Lys	290	295	300	
Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	His	Asp	305	310	315	320
Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	Tyr	Ser	Val	Gln	325	330	335	
Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	Lys	Ser	340	345	350	

Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys Phe Asp
 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
 Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
 385 390 395 400
 Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
 Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
 435 440 445
 Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
 485 490 495
 Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile Asn Asp
 500 505 510
 Gly Ser Val Ile
 515

<210> 39

<211> 1576

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (10)..(1563)

<223> Shrunk-2 gene revertant form, modified to be
heat stable

<220>

<221> variation

<222> (267)

<223> k = g or t; amino acid 86 = Ala.

<220>

<221> variation

<222> (540)

<223> n = a or g or c or t/u, unknown, or other.

<220>
 <221> variation
 <222> (1008)
 <223> y = c or t.

<220>
 <221> variation
 <222> (1197)
 <223> n = a or g or c or t/u, unknown, or other.

<220>
 <221> variation
 <222> (1368)
 <223> r = a or g; amino acid 453 = Pro.

<220>
 <221> variation
 <222> (1572)
 <223> k = g or t.

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 Met Gln Phe Ala Leu Ala Leu Asp Thr Asn Ser Gly Pro His

cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387
 Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
 115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435
 Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

130					135					140						
tcg	ctt	aac	cgc	cat	att	cat	cgt	aca	tac	ctt	gaa	ggc	ggg	atc	aac	483
Ser	Leu	Asn	Arg	His	Ile	His	Arg	Thr	Tyr	Leu	Glu	Gly	Gly	Ile	Asn	
		145					150					155				
ttt	gct	gat	gga	tct	gta	cag	gta	tta	gcg	gct	aca	caa	atg	cct	gaa	531
Phe	Ala	Asp	Gly	Ser	Val	Gln	Val	Leu	Ala	Ala	Thr	Gln	Met	Pro	Glu	
	160					165					170					
gag	cca	gtn	gga	tgg	ttc	cag	ggt	aca	gca	gac	tct	atc	aga	aaa	ttt	579
Glu	Pro	Val	Gly	Trp	Phe	Gln	Gly	Thr	Ala	Asp	Ser	Ile	Arg	Lys	Phe	
	175					180					185				190	
atc	tgg	gta	ctc	gag	gat	tat	tac	agt	cac	aaa	tcc	att	gac	aac	att	627
Ile	Trp	Val	Leu	Glu	Asp	Tyr	Tyr	Ser	His	Lys	Ser	Ile	Asp	Asn	Ile	
				195					200					205		
gta	atc	ttg	agt	ggc	gat	cag	ctt	tat	cgg	atg	aat	tac	atg	gaa	ctt	675
Val	Ile	Leu	Ser	Gly	Asp	Gln	Leu	Tyr	Arg	Met	Asn	Tyr	Met	Glu	Leu	
			210					215					220			
gtg	cag	aaa	cat	gtc	gag	gac	gat	gct	gat	atc	act	ata	tca	tgt	gct	723
Val	Gln	Lys	His	Val	Glu	Asp	Asp	Ala	Asp	Ile	Thr	Ile	Ser	Cys	Ala	
		225					230					235				
cct	gtt	gat	gag	agc	cga	gct	tct	aaa	aat	ggg	cta	gtg	aag	att	gat	771
Pro	Val	Asp	Glu	Ser	Arg	Ala	Ser	Lys	Asn	Gly	Leu	Val	Lys	Ile	Asp	
	240					245					250					
cat	act	gga	cgt	gta	ctt	caa	ttc	ttt	gaa	aaa	cca	aag	ggt	gct	gat	819
His	Thr	Gly	Arg	Val	Leu	Gln	Phe	Phe	Glu	Lys	Pro	Lys	Gly	Ala	Asp	
	255					260					265				270	
ttg	aat	tct	atg	aga	gtt	gag	acc	aac	ttc	ctg	agc	tat	gct	ata	gat	867
Leu	Asn	Ser	Met	Arg	Val	Glu	Thr	Asn	Phe	Leu	Ser	Tyr	Ala	Ile	Asp	
				275				280						285		
gat	gca	cag	aaa	tat	cca	tac	ctt	gca	tca	atg	ggc	att	tat	gtc	ttc	915
Asp	Ala	Gln	Lys	Tyr	Pro	Tyr	Leu	Ala	Ser	Met	Gly	Ile	Tyr	Val	Phe	
			290					295					300			
aag	aaa	gat	gca	ctt	tta	gac	ctt	ctc	aag	tca	aaa	tat	act	caa	tta	963
Lys	Lys	Asp	Ala	Leu	Leu	Asp	Leu	Leu	Lys	Ser	Lys	Tyr	Thr	Gln	Leu	
		305					310					315				
cat	gac	ttt	gga	tct	gaa	atc	ctc	cca	aga	gct	gta	cta	gat	cay	agt	1011
His	Asp	Phe	Gly	Ser	Glu	Ile	Leu	Pro	Arg	Ala	Val	Leu	Asp	His	Ser	
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gtg	cag	gca	tgc	att	ttt	acg	ggc	tat	tgg	gag	gat	gtt	gga	aca	atc	1059
Val	Gln	Ala	Cys	Ile	Phe	Thr	Gly	Tyr	Trp	Glu	Asp	Val	Gly	Thr	Ile	
	335					340					345				350	
aaa	tca	ttc	ttt	gat	gca	aac	ttg	gcc	ctc	act	gag	cag	cct	tcc	aag	1107

Lys Ser Phe Phe Asp Ala Asn Leu Ala Leu Thr Glu Gln Pro Ser Lys
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 Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
 370 375 380
 ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203
 Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
 385 390 395
 tca gat ggt tgc tta ctg aga gaa tgc aac atc gag cat tct gtg att 1251
 Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
 400 405 410
 gga gtc tgc tca cgt gtc agc tct gga tgt gaa ctc aag gac tcc gtg 1299
 Gly Val Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val
 415 420 425 430
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 Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
 435 440 445
 ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
 Leu Leu Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile
 450 455 460
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 Arg Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val
 465 470 475
 atc aca aac agt aag ggc atc caa gag gct gat cac ccg gaa gaa ggg 1491
 Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
 480 485 490
 tac tac ata agg tct gga atc gtg gtg atc ctg aag aat gca acc atc 1539
 Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
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<212> PRT

<213> Zea mays

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 35 40 45
 Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala Cys Pro
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 Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr Ala Asp
 65 70 75 80
 Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly Ser Gln
 85 90 95
 Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro Val Gly
 100 105 110
 Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe Asn Ser
 115 120 125
 Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr Ser Leu
 130 135 140
 Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn Phe Ala
 145 150 155 160
 Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu Glu Pro
 165 170 175
 Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe Ile Trp
 180 185 190
 Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile Val Ile
 195 200 205
 Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu Val Gln
 210 215 220
 Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala Pro Val
 225 230 235 240
 Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp His Thr
 245 250 255
 Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp Leu Asn
 260 265 270
 Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp Asp Ala
 275 280 285
 Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
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 Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu His Asp
 305 310 315 320

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Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp His Ser Val Gln
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      355                      360                      365

Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
      370                      375                      380

Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile Ser Asp
385                      390                      395                      400

Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile Gly Val
      405                      410                      415

Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
      420                      425                      430

Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu Leu Leu
      435                      440                      445

Ala Gly Lys Val Pro Val Gly Ile Gly Arg Asn Thr Lys Ile Arg Asn
      450                      455                      460

Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
465                      470                      475                      480

Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
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Gly Ser Val Ile
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<212> DNA

<213> Zea mays

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<223> Shrunk-2 gene revertant form, modified to be
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cag ata aga tct tgt gag ggt gat ggg att gac agg ttg gaa aaa tta 99
 Gln Ile Arg Ser Cys Glu Gly Asp Gly Ile Asp Arg Leu Glu Lys Leu
 15 20 25 30

agt att ggg ggc aga aag cag gag aaa gct ttg aga aat agg tgc ttt 147
 Ser Ile Gly Gly Arg Lys Gln Glu Lys Ala Leu Arg Asn Arg Cys Phe
 35 40 45

ggt ggt aga gtt gct gca act aca caa tgt att ctt acc tca gat gct 195
 Gly Gly Arg Val Ala Ala Thr Thr Gln Cys Ile Leu Thr Ser Asp Ala
 50 55 60

tgt cct gaa act ctt cat tct caa aca cag tcc tct agg aaa aat tat 243
 Cys Pro Glu Thr Leu His Ser Gln Thr Gln Ser Ser Arg Lys Asn Tyr
 65 70 75

gct gat gca aac cgt gta tct gck atc att ttg ggc gga ggc act gga 291
 Ala Asp Ala Asn Arg Val Ser Ala Ile Ile Leu Gly Gly Gly Thr Gly
 80 85 90

tct cag ctc ttt cct ctg aca agc aca aga gct acg cct gct gta cct 339
 Ser Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr Pro Ala Val Pro
 95 100 105 110

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc	387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe	
115 120 125	
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Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr	
130 135 140	
tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac	483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn	
145 150 155	
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Phe Ala Asp Gly Ser Val Gln Val Leu Ala Ala Thr Gln Met Pro Glu	
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gag cca gtn gga tgg ttc cag ggt aca gca gac tct atc aga aaa ttt	579
Glu Pro Val Gly Trp Phe Gln Gly Thr Ala Asp Ser Ile Arg Lys Phe	
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Ile Trp Val Leu Glu Asp Tyr Tyr Ser His Lys Ser Ile Asp Asn Ile	
195 200 205	
gta atc ttg agt ggc gat cag ctt tat cgg atg aat tac atg gaa ctt	675
Val Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asn Tyr Met Glu Leu	
210 215 220	
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Val Gln Lys His Val Glu Asp Asp Ala Asp Ile Thr Ile Ser Cys Ala	
225 230 235	
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Pro Val Asp Glu Ser Arg Ala Ser Lys Asn Gly Leu Val Lys Ile Asp	
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cat act gga cgt gta ctt caa ttc ttt gaa aaa cca aag ggt gct gat	819
His Thr Gly Arg Val Leu Gln Phe Phe Glu Lys Pro Lys Gly Ala Asp	
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Leu Asn Ser Met Arg Val Glu Thr Asn Phe Leu Ser Tyr Ala Ile Asp	
275 280 285	
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Asp Ala Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe	
290 295 300	
aag aaa gat gca ctt tta gac ctt ctc aag tca aaa tat act caa tta	963
Lys Lys Asp Ala Leu Leu Asp Leu Leu Lys Ser Lys Tyr Thr Gln Leu	
305 310 315	
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His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser	
320 325 330	

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355                360                365

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Phe Asp Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys
370                375                380

ttg cct ccg acg caa ttg gac aag tgc aag atg aaa tat gtn ttt atc 1203
Leu Pro Pro Thr Gln Leu Asp Lys Cys Lys Met Lys Tyr Val Phe Ile
385                390                395

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Ser Asp Gly Cys Leu Leu Arg Glu Cys Asn Ile Glu His Ser Val Ile
400                405                410

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415                420                425                430

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Met Met Gly Ala Asp Ile Tyr Glu Thr Glu Glu Glu Ala Ser Lys Leu
435                440                445

ctg tta gct ggg aag gtc ccr gtt gga ata gga agg aac aca aag ata 1395
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465                470                475

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Ile Thr Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly
480                485                490

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Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys Asn Ala Thr Ile
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<212> PRT

<213> Zea mays

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Gly  Gly  Arg  Lys  Gln  Glu  Lys  Ala  Leu  Arg  Asn  Arg  Cys  Phe  Gly  Gly
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Arg  Val  Ala  Ala  Thr  Thr  Gln  Cys  Ile  Leu  Thr  Ser  Asp  Ala  Cys  Pro
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Glu  Thr  Leu  His  Ser  Gln  Thr  Gln  Ser  Ser  Arg  Lys  Asn  Tyr  Ala  Asp
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Ala  Asn  Arg  Val  Ser  Ala  Ile  Ile  Leu  Gly  Gly  Gly  Thr  Gly  Ser  Gln
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Leu  Phe  Pro  Leu  Thr  Ser  Thr  Arg  Ala  Thr  Pro  Ala  Val  Pro  Val  Gly
          100              105              110

Gly  Cys  Tyr  Arg  Leu  Ile  Asp  Ile  Pro  Met  Ser  Asn  Cys  Phe  Asn  Ser
          115              120              125

Gly  Ile  Asn  Lys  Ile  Phe  Val  Met  Ser  Gln  Phe  Asn  Ser  Thr  Ser  Leu
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Asn  Arg  His  Ile  His  Arg  Thr  Tyr  Leu  Glu  Gly  Gly  Ile  Asn  Phe  Ala
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Asp  Gly  Ser  Val  Gln  Val  Leu  Ala  Ala  Thr  Gln  Met  Pro  Glu  Glu  Pro
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Val  Gly  Trp  Phe  Gln  Gly  Thr  Ala  Asp  Ser  Ile  Arg  Lys  Phe  Ile  Trp
          180              185              190

Val  Leu  Glu  Asp  Tyr  Tyr  Ser  His  Lys  Ser  Ile  Asp  Asn  Ile  Val  Ile
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Leu  Ser  Gly  Asp  Gln  Leu  Tyr  Arg  Met  Asn  Tyr  Met  Glu  Leu  Val  Gln
          210              215              220

Lys  His  Val  Glu  Asp  Asp  Ala  Asp  Ile  Thr  Ile  Ser  Cys  Ala  Pro  Val
          225              230              235              240

Asp  Glu  Ser  Arg  Ala  Ser  Lys  Asn  Gly  Leu  Val  Lys  Ile  Asp  His  Thr
          245              250              255

Gly  Arg  Val  Leu  Gln  Phe  Phe  Glu  Lys  Pro  Lys  Gly  Ala  Asp  Leu  Asn
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Ser  Met  Arg  Val  Glu  Thr  Asn  Phe  Leu  Ser  Tyr  Ala  Ile  Asp  Asp  Ala
          275              280              285

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Gln Lys Tyr Pro Tyr Leu Ala Ser Met Gly Ile Tyr Val Phe Lys Lys
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 305 310 315 320
 Phe Gly Ser Glu Ile Leu Pro Arg Ala Val Leu Asp Tyr Ser Val Gln
 325 330 335
 Ala Cys Ile Phe Thr Gly Tyr Trp Glu Asp Val Gly Thr Ile Lys Ser
 340 345 350
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 355 360 365
 Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr Ala Pro Arg Cys Leu Pro
 370 375 380
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 385 390 395 400
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 405 410 415
 Cys Ser Arg Val Ser Ser Gly Cys Glu Leu Lys Asp Ser Val Met Met
 420 425 430
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 435 440 445
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 450 455 460
 Cys Ile Ile Asp Met Asn Ala Arg Ile Gly Lys Asn Val Val Ile Thr
 465 470 475 480
 Asn Ser Lys Gly Ile Gln Glu Ala Asp His Pro Glu Glu Gly Tyr Tyr
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Pro Met Ile Val Ser Pro Lys Ala Val Ser Asp Ser Gln Asn Ser Gln	65	70	75
Thr Cys Leu Asp Pro Asp Ala Ser Arg Ser Val Leu Gly Ile Ile Leu	85	90	95
Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys Arg Ala	100	105	110
Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp Ile Pro	115	120	125
Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val Leu Thr	130	135	140
Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala Tyr Ala	145	150	155
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Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Thr Val Leu Glu	195	200	205
Tyr Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr Glu Lys	210	215	220
Phe Ile Gln Ala His Arg Glu Thr Asp Ala Asp Ile Thr Val Ala Ala	225	230	235
Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met Lys Ile	245	250	255
Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Gln Gly Glu	260	265	270
Gln Leu Gln Ala Met Lys Val Asp Thr Thr Ile Leu Gly Leu Asp Asp	275	280	285
Lys Arg Ala Lys Glu Met Pro Phe Ile Ala Ser Met Gly Ile Tyr Val	290	295	300


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Met Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp Ile Gly
                      340                      345                      350

Thr Ile Glu Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys Lys Pro
                      355                      360                      365

Val Pro Asp Phe Ser Phe Tyr Asp Arg Ser Ala Pro Ile Tyr Thr Gln
370                      375                      380

Pro Arg Tyr Leu Pro Pro Ser Lys Met Leu Asp Ala Asp Val Thr Asp
385                      390                      395                      400

Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile His His
                      405                      410                      415

Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile Ile Glu
420                      425                      430

Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Asp Ala Asp Arg
435                      440                      445

Lys Leu Leu Ala Ala Lys Gly Ser Val Pro Ile Gly Ile Gly Lys Asn
450                      455                      460

Cys His Ile Lys Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile Gly Asp
465                      470                      475                      480

Asn Val Lys Ile Ile Asn Lys Asp Asn Val Gln Glu Ala Ala Arg Glu
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20           25           30

Xaa Xaa Xaa Xaa Ala Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35           40           45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50           55           60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa
65           70           75           80

Thr Xaa Leu Xaa Pro Xaa Ala Xaa Xaa Ser Val Leu Gly Ile Ile Leu
85           90           95

Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys Arg Ala
100          105          110

Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp Ile Pro
115          120          125

Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val Leu Thr
130          135          140

Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala Tyr Ala
145          150          155          160

Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val Leu Ala
165          170          175

Ala Gln Gln Ser Pro Asp Asn Pro Xaa Trp Phe Gln Gly Thr Ala Asp
180          185          190

Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Xaa Val Leu Glu
195          200          205

Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr Glu Lys
210          215          220

Phe Ile Gln Ala His Arg Glu Thr Xaa Ala Asp Ile Thr Val Ala Ala
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Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met Lys Ile
245          250          255

Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Xaa Gly Glu
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Gln Leu Xaa Ala Met Xaa Val Asp Thr Thr Ile Leu Gly Leu Asp Asp
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Xaa Arg Ala Lys Glu Met Pro Phe Ile Ala Ser Met Gly Ile Tyr Val

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		500						505					510		
Ala	Leu	Ile	Pro	Ser	Gly	Xaa	Ile	Ile							
	515						520								